



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

<b>Code(s) assigned:</b>	<b>2008.001-004,6I</b>	(to be completed by ICTV officers)
<b>Short title:</b> Creation of a new genus in Dicistroviridae and addition of a new species to the genus (e.g. 6 new species in the genus <i>Zetavirus</i> ; re-classification of the family <i>Zetaviridae</i> etc.)		
<b>Modules attached</b> (please check all that apply):	1 <input type="checkbox"/>	2 <input type="checkbox"/>
	3 <input type="checkbox"/>	4 <input checked="" type="checkbox"/>
	5 <input checked="" type="checkbox"/>	6 <input type="checkbox"/>
	7 <input type="checkbox"/>	

**Author(s) with e-mail address(es) of the proposer:**

Dicistroviridae Study Group:  
Nobuhiko Nakashima (nakaji@affrc.go.jp), Karyn Johnson (karynj@uq.edu.au); Frank van der Wilk (Frank.van.der.Wilk@rivm.nl); Les Domier: (l-domier@uiuc.edu); Peter Christian (pchristian@nibsc.ac.uk); Judy Chen (ChenJ@ba.ars.usda.gov) ; Tamas Bakonyi (Bakonyi.Tamas@aotk.szie.hu).

**ICTV-EC or Study Group comments and response of the proposer:**

Accepted in principal by the EC, with the decision to fast-track the proposal for *Homalodisca coagulata virus-1*. The only comment from the EC was that it would be useful to include a phenogram for the proposed generic division based on the replicase as well as the CP

SG: Corrections made and proposal for *Homalodisca coagulata virus-1* removed (now 2008.005I).

MODULE 4: **NEW GENUS** (if more than one genus is to be created, please complete additional copies of this section)

Code	<b>2008.001I</b>	(assigned by ICTV officers)
<b>To create a new genus assigned as follows:</b>		
Subfamily:		Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put "unassigned" here.
Family:	<i>Dicistroviridae</i>	
Order:	<i>Picornavirales</i>	

Code	<b>2008.002I</b>	(assigned by ICTV officers)
<b>To name the new genus:</b> <i>Aparavirus</i>		

Code	<b>2008.003I</b>	(assigned by ICTV officers)
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**To assign the following as species in the new genus:**

You may list several species here. For each species, please state whether it is new or existing.

- If the species is new, please complete Module 5 to create it.
- If the species already exists, please state whether it is unassigned or is to be removed from another genus and, if the latter, complete module 6(a) to 'REMOVE' it from that genus.

*Acute bee paralysis virus*

*Israeli acute paralysis virus* (New Species See Module 5)

*Kashmir bee virus*

*Solenopsis invicta virus-1*

*Taura syndrome virus*

Code **2008.0041** (assigned by ICTV officers)

Note: every genus must have a type species

**To designate the following as the type species in the new genus:**

*Acute bee paralysis virus*

**Argument to justify the creation of a new genus:**

All 14 members of the family *Dicistroviridae* infect invertebrates. The positive-sense RNA genome of dicistroviruses encode two large open reading frames. The dicistrovirus genome is characterized by the presence of an internal ribosome entry site (IRES) at the intergenic region (IGR) between the two ORFs.

The structure of the IGR-IRES of known dicistroviruses can be divided into two classes. One class is composed of members of the genus *Cripavirus* while the other includes the viruses recommended to form the *Aparavirus* genus. The typical IRES of cripaviruses have conserved bulge sequence (UGAUCU and UGC) while the members in the created genus *Aparavirus* have different bulge sequence (UGGUUACCCA and UAAGGCUU) (Figure 1). In addition, the structure of the IRES elements in the two genera are also distinguished by the presence of an additional stem loop in the 3' region of the IGR-IRES of the *aparaviruses* but not in *cripaviruses* (Figure 1).

Phylogenetic analysis of deduced amino acid sequence of capsid protein precursors and the RNA-dependent RNA polymerase also indicates that *cripaviruses* and *aparaviruses* form distinct groups in the family (Figure 2).

**Origin of the new genus name:**

*Apara*: sigla from the type member of the genus '*Acute bee paralysis virus*'.

**Argument to justify the choice of type species:**

Among members in the new genus *Acute bee paralysis virus* was the first described virus (Bailey et al., 1963) and complete sequence data are available for this virus.

**Species demarcation criteria in the genus:**

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

**Species demarcation criteria in the genus:**

The primary species demarcation criteria (as for the genus *Cripavirus*) is :

1. Sequence identity between the capsid proteins of isolates and strains of a species is above 90%.

In addition, where reagents/data are available the following may also be used:

2. Natural host range: species can be differentiated on the basis of their natural host range and their relative ability to replicate in a range of cultured insect cells.

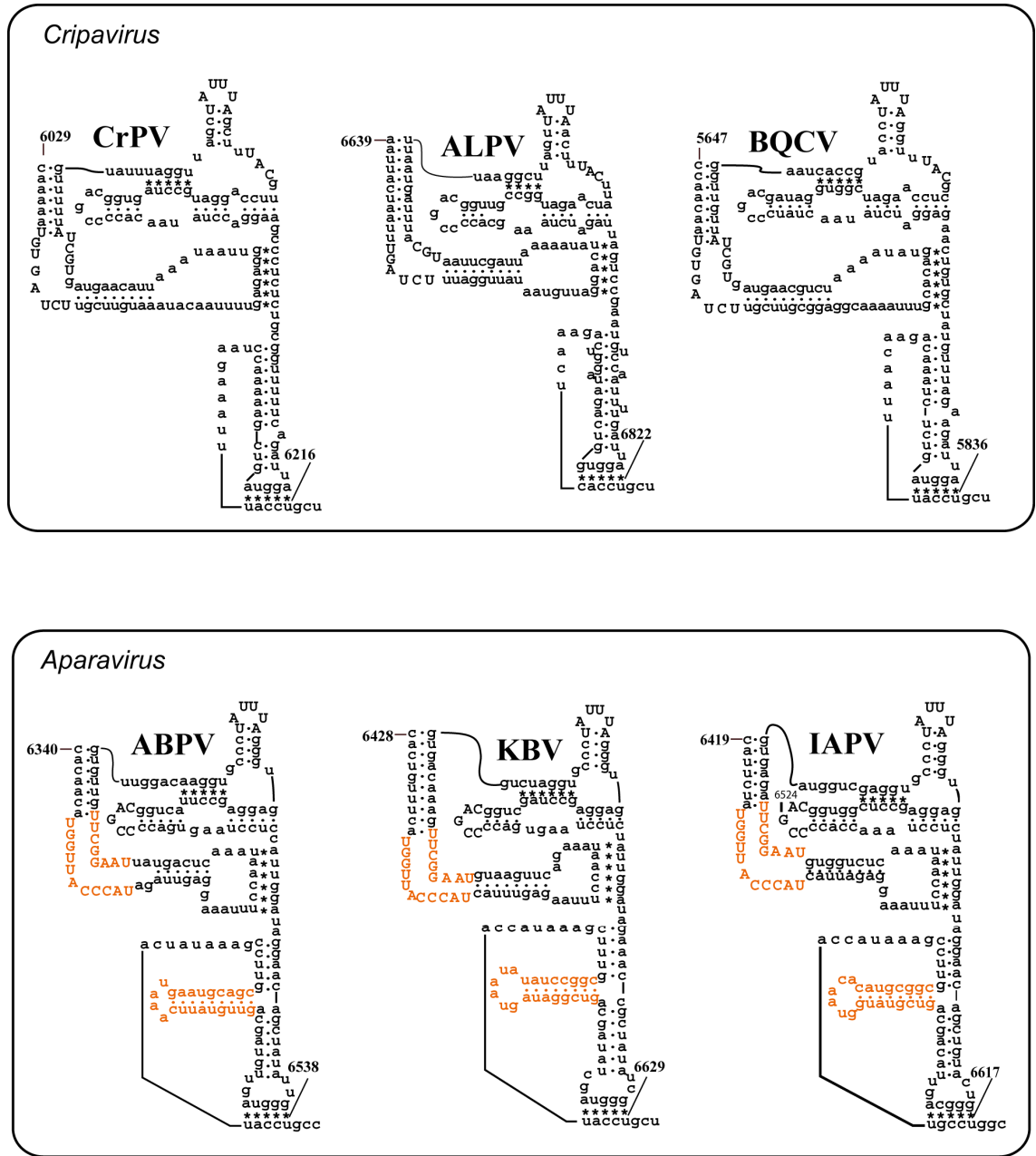
3. Serology: species are serologically distinct.

**References:**

- Bailey, L., Gibbs, A.J, Woods, R.D. (1963) Two viruses from adult honey bees (*Apis mellifera* Linnaeus). *Virology* 21, 390-395.
- de Miranda, J.R., Drebot, M., Tyler, S., Shen, M., Cameron, C.E., Stoltz, D.B. and Camazine, S.M. (2004) Complete nucleotide sequence of Kashmir bee virus and comparison with acute bee paralysis virus. *J Gen Virol* 85, 2263-2270.
- Maori, E., Lavi, S., Mozes-Koch, R., Gantman, Y., Peretz, Y., Edelbaum, O., Tanne, E. and Sela, I. (2007) Isolation and characterization of Israeli acute paralysis virus, a dicistrovirus affecting honeybees in Israel: evidence for diversity due to intra- and inter-species recombination. *J Gen Virol* 88, 3428-3438.
- Valles, S.M., Strong, C.A., Oi, D.H., Porter, S.D., Pereira, R.M., Vander Meer, R.K., Hashimoto, Y., Hooper-Bui, L.M., Sanchez-Arroyo, H., Davis, T., Karpakakunjaram, V., Vail, K.M., Fudd Graham, L.C., Briano, J.A., Calcaterra, L.A., Gilbert, L.E., Ward, R., Ward, K., Oliver, J.B., Taniguchi, G. and Thompson, D.C. (2007) Phenology, distribution, and host specificity of *Solenopsis invicta* virus-1. *J Invertebr Pathol* 96, 18-27.
- Valles, S.M., Strong, C.A., Dang, P.M., Hunter, W.B., Pereira, R.M., Oi, D.H., Shapiro, A.M. and Williams, D.F. (2004) A picorna-like virus from the red imported fire ant, *Solenopsis invicta*: initial discovery, genome sequence, and characterization. *Virology* 328, 151-157.
- Mari, J., Poulos, B.T., Lightner, D.V. and Bonami, J.R. (2002) Shrimp Taura syndrome virus: genomic characterization and similarity with members of the genus Cricket paralysis-like viruses. *J Gen Virol* 83, 915-926.
- Govan, V.A., Leat, N., Allsopp, M. and Davison, S. (2000) Analysis of the complete genome sequence of acute bee paralysis virus shows that it belongs to the novel group of insect-infecting RNA viruses. *Virology* 277, 457-463.
- Hatakeyama, Y., Shibuya, N., Nishiyama, T. and Nakashima, N.(2004) Structural variant of the intergenic internal ribosome entry site elements in dicistroviruses and computational search for their counterparts. *RNA* 10, 779-786.
- Cevallos, R.C. and Sarnow, P.(2005) Factor-independent assembly of elongation-competent ribosomes by an internal ribosome entry site located in an RNA virus that infects penaeid shrimp. *J. Virol.* 179, 677-683.
- Pfingsten, J.S., Costantino, D.A. and Kieft, J.S. (2007) Conservation and diversity among the three-dimensional folds of the Dicistroviridae intergenic region IRESes. *J. Mol. Biol.* 370, 856-869.

**Annexes:**

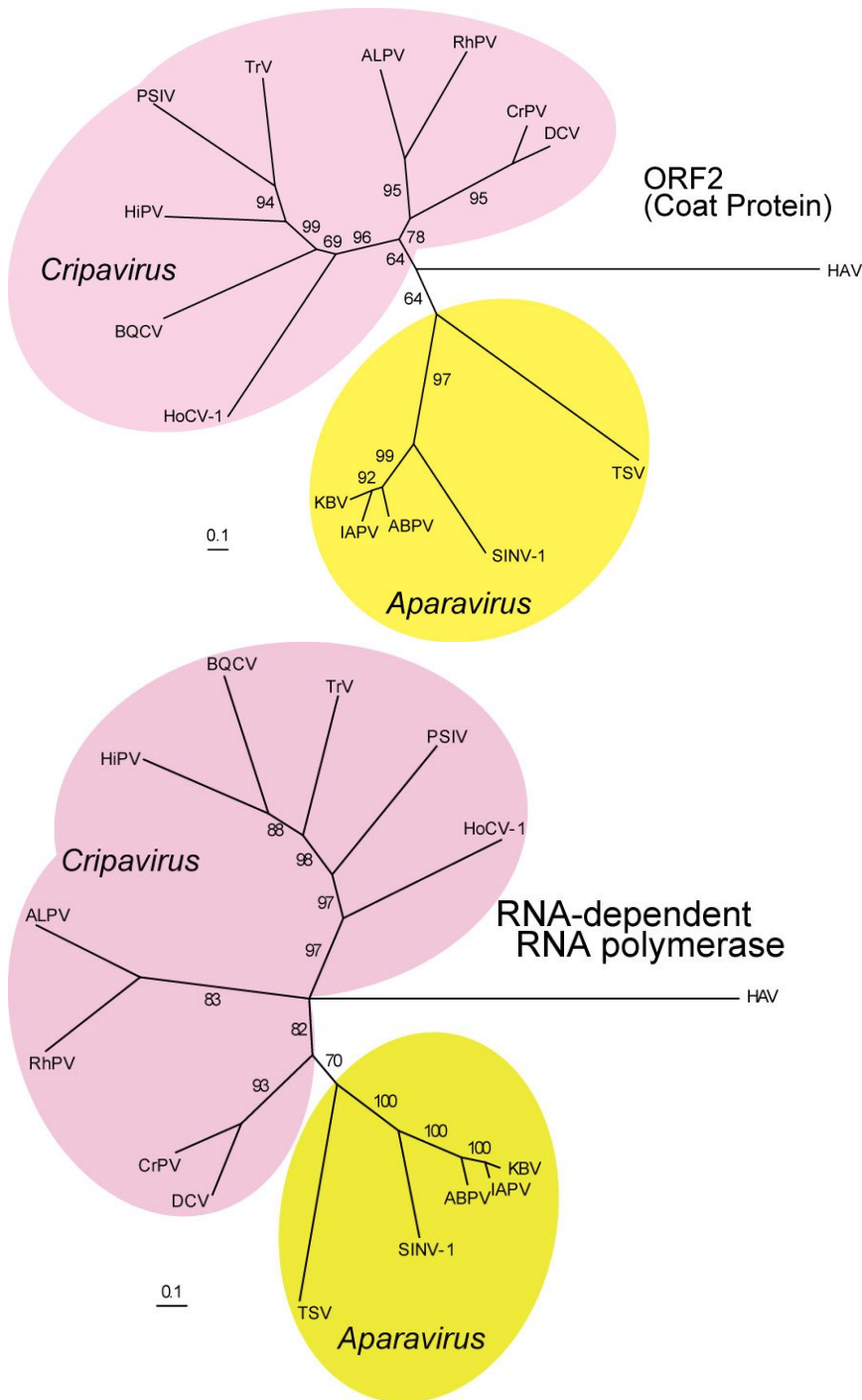
Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.



**Figure 1**

Structure of IGR-IRES elements. Typical structures observed in aparaviruses are shown in orange. Additional stem loop structures and nucleotide sequences in the bulge regions are shared by the genus members, ABPV, KBV, SINV-1, and TSV.

Data on isolates of the newly proposed species Israeli acute paralysis virus (IAPV) (*Aparavirus*) is also included in this figure (see Module 5).



**Figure 2.**

Neighbour joining trees constructed from alignments of the deduced amino acid sequences of structural proteins encoding ORF2 (coat protein) and RNA-dependent RNA polymerase (RdRP) of dicistroviruses. Deduced amino acid sequences for capsid protein precursor and RdRP of hepatitis A virus were used for outgroup. Cripaviruses: ALPV, aphid lethal paralysis virus, AF536531; BQCV, black queen-cell virus, AF183905; CrPV, cricket paralysis virus, AF218039; DCV, Drosophila C virus, AF014388; HiPV, himetobi P virus, AB017037; HoCV-1, Homalodisca coagulata virus-1, DQ288865; PSIV, Plautia stali intestine virus, AB006531; RhPV, Rhopalosiphum padi virus, AF022937; TrV, Triatoma virus, AF178440. Aparaviruses; ABPV, acute bee paralysis virus, AF150629; IAPV, Israeli

acute paralysis virus, EF219380; KBV, Kashmir bee virus, AY275710; SiNV-1, Solenopsis invicta virus-1, AY634314; TSV, Taura syndrome virus, AF277675.

Data on isolates of the newly proposed species in the family: Homoldisca coagulata virus-1 (HoCV-1) (*Cripavirus*) and Israeli acute paralysis virus (IAPV) (*Aparavirus*) are also included in this figure (see Module 5).

MODULE 5: **NEW SPECIES**

Code	<b><i>2008.006I</i></b>	(assigned by ICTV officers)
<b>To create <i>Israeli acute paralysis virus</i> ; a new species assigned as follows:</b>		
Genus:	<i>Aparavirus</i>	Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put “unassigned” in the genus box)
Subfamily:		
Family:	<i>Dicistroviridae</i>	
Order:	<i>Picornavirales</i>	

**Name(s) of proposed new species:**

Dicistroviridae Study Group:  
 Nobuhiko Nakashima (nakaji@affrc.go.jp), Karyn Johnson (karynj@uq.edu.au);  
 Frank van der Wilk (Frank.van.der.Wilk@rivm.nl); Les Domier: (l-domier@uiuc.edu); Peter Christian (pchristian@nibsc.ac.uk); Judy Chen  
 (ChenJ@ba.ars.usda.gov) ; Tamas Bakonyi (Bakonyi.Tamas@aotk.szie.hu).

**Argument to justify the creation of the new species:**

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Whole genome sequence [EF219380] of Israeli acute paralysis virus (IAPV) was reported by Maori et al. (2007). This virus has a monopartite positive-sense RNA genome with two non-overlapping open reading frames (ORFs), that encode the nonstructural polyproteins in the 5' ORF and structural proteins in the 3' ORF.  
 Overall the genome organization of IAPV is typical of the family *Dicistroviridae*. The intergenic region of the genome of IAPV is however, predicted to form a secondary structure similar to ABPV and other viruses proposed as members of a new genus, *Aparavirus* (see Module 4 – Figure 1).  
 Phylogenetic analysis shows that IAPV clusters with other proposed members of the newly proposed genus, *Aparavirus* (Figure 2)

**References:**

Maori, E., Lavi, S., Mozes-Koch, R., Gantman, Y., Peretz, Y., Edelbaum, O., Tanne, E. and Sela, I. (2007) Isolation and characterization of Israeli acute paralysis virus, a dicistrovirus affecting honeybees in Israel: evidence for diversity due to intra- and inter-species recombination. *J. Gen. Virol.* **88**, 3428-3438.

